1644

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/812,393A*

DATE: 07/07/98
TIME: 09:45:43

INPUT SET: S27223.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                                   SEQUENCE LISTING        ENTERED
 2
 3   (1)     General Information
 4
 5           (i) APPLICANT: SHERMAN, Linda A.
 6                          LUSTGARTEN, Joseph
 7
 8           (ii) TITLE OF THE INVENTION: RECOMBINANT CONSTRUCTS ENCODING
 9                    T CELL RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR
10                    ANTIGENS
11
12           (iii) NUMBER OF SEQUENCES: 64
13
14           (iv) CORRESPONDENCE ADDRESS:
15              (A) ADDRESSEE: MORRISON & FOERSTER
16              (B) STREET: 2000 Pennsylvania Avenue, NW, suite 5500
17              (C) CITY: Washington
18              (D) STATE: DC
19              (E) COUNTRY: USA
20              (F) ZIP: 20006-1888
21
22           (v) COMPUTER READABLE FORM:
23              (A) MEDIUM TYPE: Diskette
24              (B) COMPUTER: IBM Compatible
25              (C) OPERATING SYSTEM: DOS
26              (D) SOFTWARE: FastSEQ for Windows Version 2.0
27
28           (vi) CURRENT APPLICATION DATA:
29              (A) APPLICATION NUMBER: 08/812,393
30              (B) FILING DATE: 05-MAR-1997
31              (C) CLASSIFICATION:
32
33           (vii) PRIOR APPLICATION DATA:
34              (A) APPLICATION NUMBER:
35              (B) FILING DATE:
36
37
38
39           (viii) ATTORNEY/AGENT INFORMATION:
40              (A) NAME: Murashige, Kate H
41              (B) REGISTRATION NUMBER: 29,959
42              (C) REFERENCE/DOCKET NUMBER: 31333-20001.00
43
44           (ix) TELECOMMUNICATION INFORMATION:
45              (A) TELEPHONE: 202-887-1500
46              (B) TELEFAX: 202-822-0168
```

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47            (C) TELEX:
48
49
50         (2) INFORMATION FOR SEQ ID NO:1:
51
52      (i) SEQUENCE CHARACTERISTICS:
53         (A) LENGTH: 1350 base pairs
54         (B) TYPE: nucleic acid
55         (C) STRANDEDNESS: double
56         (D) TOPOLOGY: linear
57
58      (ix) FEATURE:
59
60         (A) NAME/KEY: Coding Sequence
61         (B) LOCATION: 1...1332
62         (D) OTHER INFORMATION:
63
64      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
65
66   CTC GAG ATG CAG AGG AAC CTG GGA GCT GTG CTG GGG ATT CTG TGG GTG        48
67   Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
68    1           5                   10                  15
69
70   CAG ATT TGC TGG CTG AAA GAA CAG CAA GTG CAG CAG AGT CCC GCA TCC        96
71   Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
72            20                  25                  30
73
74   TTG GTT CTG CAG GAG GGG GAG AAC GCA GAG CTC CAG TGT AGC TTT TCC       144
75   Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
76            35                  40                  45
77
78   ATC TTT ACA AAC CAG GTG CAG TGG TTT TAC CAA CGT CCT GGG GGA AGA       192
79   Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
80            50                  55                  60
81
82   CTC GTC AGC CTG TTG TAC AAT CCT TCT GGG ACA AAG CAG AGT GGG AGA       240
83   Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
84   65                  70                  75                  80
85
86   CTG ACA TCC ACA ACA GTC ATT AAA GAA CGT CGC AGC TCT TTG CAC ATT       288
87   Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
88            85                  90                  95
89
90   TCC TCC TCC CAG ATC ACA GAC TCA GGC ACT TAT CTC TGT GCC TCA AAT       336
91   Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
92            100                 105                 110
93
94   TCT GGA GGA AGC AAT GCA AAG CTA ACC TTC GGG AAA GGC ACT AAA CTC       384
95   Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
96            115                 120                 125
97
98   TCT GTT AAA TCA GGT GGC GGA GGG TCT GGC GGG GGT GGA TCC GGG GGT       432
99   Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
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100        130                    135                    140
101
102    GGA GGC TCA GAG GCT GCA GTC ACC CAA AGC CCA AGA AAC AAG GTG GCA        480
103    Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
104    145                150                    155                    160
105
106    GTA ACA GGA GGA AAG GTG ACA TTG AGC TGT AAT CAG ACT AAT AAC CAC        528
107    Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
108                       165                    170                    175
109
110    AAC AAC ATG TAC TGG TAT CGG CAG GAC ACG GGG CAT GGG CTG AGG CTG        576
111    Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
112                       180                    185                    190
113
114    ATC CAT TAT TCA TAT GGT GCT GGC AGC ACT GAG AAA GGA GAT ATC CCT        624
115    Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
116                       195                    200                    205
117
118    GAT GGA TAC AAG GCC TCC AGA CCA AGC CAA GAG AAC TTC TCC CTC ATT        672
119    Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile
120             210                    215                    220
121
122    CTG GAG TTG GCT ACC CCC TCT CAG ACA TCA GTG TAC TTC TGT GCC AGC        720
123    Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
124    225                230                    235                    240
125
126    GGT GAG ACA GGG ACC AAC GAA AGA TTA TTT TTC GGT CAT GGA ACC AAG        768
127    Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
128                       245                    250                    255
129
130    CTG TCT GTC CTG ACT AGT AAC TCC ATC ATG TAC TTC AGC CAC TTC GTG        816
131    Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
132                       260                    265                    270
133
134    CCG GTC TTC CTG CCA GCG AAG CCC ACC ACG ACG CCA GCG CCG CGA CCA        864
135    Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
136             275                    280                    285
137
138    CCA ACA CCG GCG CCC ACC ATC GCG TCG CAG CCC CTG TCC CTG CGC CCA        912
139    Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
140             290                    295                    300
141
142    TCT AGT TCT AGA GAT CCC AAA CTC TGC TAC CTG CTG GAT GGA ATC CTC        960
143    Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
144    305                310                    315                    320
145
146    TTC ATC TAT GGT GTC ATT CTC ACT GCC TTG TTC CTG AGA GTG AAG TTC        1008
147    Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
148                       325                    330                    335
149
150    AGC AGG AGC GCA GAC GCC CCC GCG TAC CAG CAG GGC CAG AAC CAG CTC        1056
151    Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
152             340                    345                    350
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153
154     TAT AAC GAG CTC AAT CTA GGA CGA AGA GAG GAG TAC GAT GTT TTG GAC      1104
155     Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
156          355                 360                 365
157
158     AAG AGA CGT GGC CGG GAC CCT GAG ATG GGG GGA AAG CCG AGA AGG AAG      1152
159     Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
160          370                 375                 380
161
162     AAC CCT CAG GAA GGC CTG TAC AAT GAA CTG CAG AAA GAT AAG ATG GCG      1200
163     Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
164     385                 390                 395                 400
165
166     GAG GCC TAC AGT GAG ATT GGG ATG AAA GGC GAG CGC CGG AGG GGC AAG      1248
167     Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
168                     405                 410                 415
169
170     GGG CAC GAT GGC CTT TAC CAG GGT CTC AGT ACA GCC ACC AAG GAC ACC      1296
171     Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
172                     420                 425                 430
173
174     TAC GAC GCC CTT CAC ATG CAG GCC CTG CCC CCT CGC TAAGCGGCCG CCACCG    1348
175     Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
176                     435                 440
177
178     CG                                                                  1350
179
180          (2) INFORMATION FOR SEQ ID NO:2:
181
182          (i) SEQUENCE CHARACTERISTICS:
183             (A) LENGTH: 444 amino acids
184             (B) TYPE: amino acid
185             (C) STRANDEDNESS: single
186             (D) TOPOLOGY: linear
187
188          (ii) MOLECULE TYPE: protein
189          (v) FRAGMENT TYPE: internal
190
191          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
192
193     Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
194      1                 5                 10                  15
195     Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
196                     20                  25                  30
197     Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
198                     35                  40                  45
199     Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
200          50                  55                  60
201     Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
202     65                  70                  75                  80
203     Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
204                     85                  90                  95
205     Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
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INPUT SET: S27223.raw

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206                  100                 105                 110
207     Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
208              115                 120                 125
209     Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
210              130                 135                 140
211     Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
212     145                 150                 155                 160
213     Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
214                  165                 170                 175
215     Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
216              180                 185                 190
217     Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
218              195                 200                 205
219     Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile
220              210                 215                 220
221     Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
222     225                 230                 235                 240
223     Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
224                  245                 250                 255
225     Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
226              260                 265                 270
227     Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
228              275                 280                 285
229     Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
230              290                 295                 300
231     Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
232     305                 310                 315                 320
233     Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
234              325                 330                 335
235     Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
236              340                 345                 350
237     Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
238              355                 360                 365
239     Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
240              370                 375                 380
241     Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
242     385                 390                 395                 400
243     Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
244              405                 410                 415
245     Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
246              420                 425                 430
247     Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
248              435                 440
249
250          (2) INFORMATION FOR SEQ ID NO:3:
251
252          (i) SEQUENCE CHARACTERISTICS:
253             (A) LENGTH: 24 base pairs
254             (B) TYPE: nucleic acid
255             (C) STRANDEDNESS: single
256             (D) TOPOLOGY: linear
257
258          (vi) ORIGINAL SOURCE:
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/812,393A*

INPUT SET: S27223.raw

Line	Error	Original Text